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[illegible]



```
3050 AACACCATGCCGAGAGTAAAAACAACACGAGAGTAGCAGCACAGTAC 3099
491 ..... GluGlnLeuAspTyrL 496
3100 GAGTAACACACAAAGCGCTGGAGTGCACATGAGGAGCAGCTCTGTACC 3149
496 euSerArgValGlnGlyPheGlnValGluTyrLysAspPheProLysAsn 512
3150 TTACTAAACTCTGAGCTTGTAGGTCAACTCTCGACTATCCGAAAGGC 3199
513 AsnLysAsnGluPheValSerLeuIleAsnCysSerSerGlnProIole 529
3200 AATGCACAAGGTTCTGACCATCTGATGTCACACATCCGCCGCA 3249
529 uIleSerHisGlyIleGlyLysAspValGluSerCysHisAspMetAla 546
3250 GATTGCCATGGCGCTTGCCAAAGACCTCCGAGGAGTCGCGAATGATGCTG 3299
546 AlaLeuAsnIleLeuLysLeuLeuSerGlnLeu 556
3300 CAAGCAATGCCCTTGAAAAATCTCTCAGCAAGCTG 3331
```









RESULT	13
LOCUS	AL158850/c
DEFINITION	AL158850 192597 bp DNA HTG 06-SEP-2000
ACCESSION	AL158850
VERSION	AL158850.4 GI:9800143
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 192597)
JOURNAL	Burton, J.
COMMENT	Direct Submission Submitted (05-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk On Aug 13, 2000 this sequence version replaced gi:9212635.

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Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humphreys@sanger.ac.uk
----- Project Information
Center project name: d3522219
----- Summary Statistics
Assembly program: XGAP4, version 4.5
Sequencing vector: M13; M77815; 12% of reads
Sequencing vector: plasmid; L08752; 87% of reads
Chemistry: Dye-terminator Big Dye; 77% of reads
Chemistry: Dye-terminator-mercam; 22% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 185625 bases at least Q40
Consensus quality: 18853 bases at least Q30
Consensus quality: 190005 bases at least Q20
Insert size: 191597; sum-of-contigs
Insert size: 144116; 9.6% error; agarose-fp
Quality coverage: 5.71x in Q20 bases; sum-of-contigs Quality

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coverage: 8.21x in Q20 bases; agarose-ip
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 13837: contig of 13837 bp in length
*
* 13838 13937: gap of 100 bp
*
* 13938 17476: contig of 3539 bp in length
*
* 17477 17576: gap of 100 bp
*
* 17577 20005: contig of 2429 bp in length
*
* 20006 20105: gap of 100 bp
*
* 20106 32070: contig of 11965 bp in length
*
* 32071 32170: gap of 100 bp
*
* 32171 39772: contig of 7602 bp in length
*
* 39773 39872: gap of 100 bp
*
* 39873 43471: contig of 3599 bp in length
*
* 43472 43571: gap of 100 bp
*
* 43572 51795: contig of 8224 bp in length
*
* 51796 51895: gap of 100 bp
*
* 51896 178838: contig of 126943 bp in length
*
* 178839 178938: gap of 100 bp
*
* 178939 181819: contig of 2981 bp in length
*
* 181820 182019: gap of 100 bp
*
* 182020 184231: contig of 2212 bp in length
*
* 184232 184331: gap of 100 bp
*
* 184332 192597: contig of 8266 bp in length.
*
Location/Qualifiers
1..192597

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	Query Match	11.4%	Score 383.2	DB 70	Length 192597
misc_feature	178939..181319	/note="assembly-fragment:01637"			
misc_feature	182020..184231	/note="assembly-fragment:02408"			
misc_feature	184332..192597	/note="assembly-fragment:02960"			
BASE COUNT	58324 a 39515 c 38313 g 55431 t 1014	others			
ORIGIN					